

## GeDiPNet Cluster 106 -- Enriched Pathways

Pathway enrichment: KEGG + Reactome, upper-tail hypergeometric test, Benjamini-Hochberg FDR-corrected. Fold enrichment = (overlap / cluster gene count) / (pathway gene count / universe size). Top 15 pathways per cluster by q-value. See [scripts/build\\_cluster\\_enrichment.php](#) on [gedipnet.bicnirrh.res.in](#). Data as of: 2026-10-10 03:30:08. · Rows: 15 · Generated: 2026-10-09 22:01:25

| Pathway                                                    | Source   | Overlap Genes | Overlap Gene Names                              | Pathway Gene Count | Cluster Gene Count | Fold Enrichment | P-value   | FDR Q-value |
|------------------------------------------------------------|----------|---------------|-------------------------------------------------|--------------------|--------------------|-----------------|-----------|-------------|
| Cobalamin (Cbl, vitamin B12) transport and metabolism      | Reactome | 8             | AMN, CUBN, TCN1, TCN2, CD320, MMAA, MMUT, ABCD4 | 21                 | 37                 | 123.66          | 7.133e-16 | 2.679e-13   |
| Cobalamin transport and metabolism                         | KEGG     | 6             | TCN1, TCN2, CD320, MMAA, MMUT, ABCD4            | 18                 | 37                 | 108.20          | 1.010e-11 | 1.837e-9    |
| Vitamin digestion and absorption                           | KEGG     | 6             | AMN, CUBN, SLC19A2, TCN2, SLC19A1, ABCD4        | 26                 | 37                 | 74.91           | 1.230e-10 | 1.778e-8    |
| Glycosphingolipid biosynthesis - lacto and neolacto series | KEGG     | 4             | FUT1, FUT2, FUT3, FUT6                          | 28                 | 37                 | 46.37           | 1.480e-6  | 7.374e-5    |
| Vitamin D (calciferol) metabolism                          | Reactome | 3             | CUBN, CYP2R1, GC                                | 11                 | 37                 | 88.53           | 4.367e-6  | 1.820e-4    |
| Defective MMAA causes methylmalonic aciduria type cblA     | Reactome | 2             | MMAA, MMUT                                      | 2                  | 37                 | 324.59          | 9.235e-6  | 3.326e-4    |
| Defective MUT causes methylmalonic aciduria mut type       | Reactome | 2             | MMAA, MMUT                                      | 2                  | 37                 | 324.59          | 9.235e-6  | 3.326e-4    |
| Defective CD320 causes methylmalonic aciduria              | Reactome | 2             | TCN2, CD320                                     | 2                  | 37                 | 324.59          | 9.235e-6  | 3.326e-4    |
| Metabolism of folate and pterines                          | Reactome | 3             | DHFR, MTHFR, SLC19A1                            | 17                 | 37                 | 57.28           | 1.777e-5  | 5.698e-4    |
| Lewis blood group biosynthesis                             | Reactome | 3             | FUT2, FUT3, FUT6                                | 18                 | 37                 | 54.10           | 2.128e-5  | 6.647e-4    |
| ABO blood group biosynthesis                               | Reactome | 2             | FUT1, FUT2                                      | 3                  | 37                 | 216.40          | 2.765e-5  | 8.242e-4    |
| Defective AMN causes hereditary megaloblastic anemia 1     | Reactome | 2             | AMN, CUBN                                       | 3                  | 37                 | 216.40          | 2.765e-5  | 8.242e-4    |
| Defective CUBN causes hereditary megaloblastic anemia 1    | Reactome | 2             | AMN, CUBN                                       | 3                  | 37                 | 216.40          | 2.765e-5  | 8.242e-4    |
| Propionyl-CoA catabolism                                   | Reactome | 2             | MMAA, MMUT                                      | 5                  | 37                 | 129.84          | 9.182e-5  | 2.165e-3    |
| HDL clearance                                              | Reactome | 2             | AMN, CUBN                                       | 5                  | 37                 | 129.84          | 9.182e-5  | 2.165e-3    |